

1/41

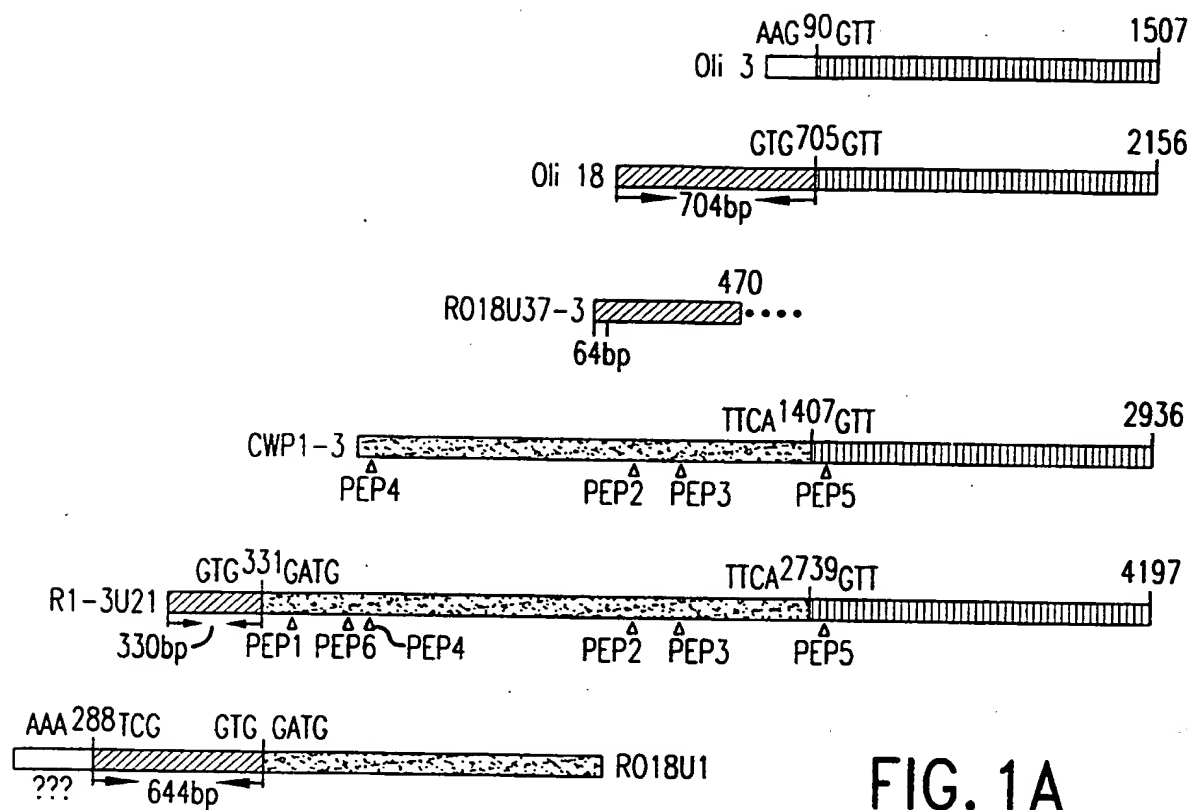


FIG. 1A

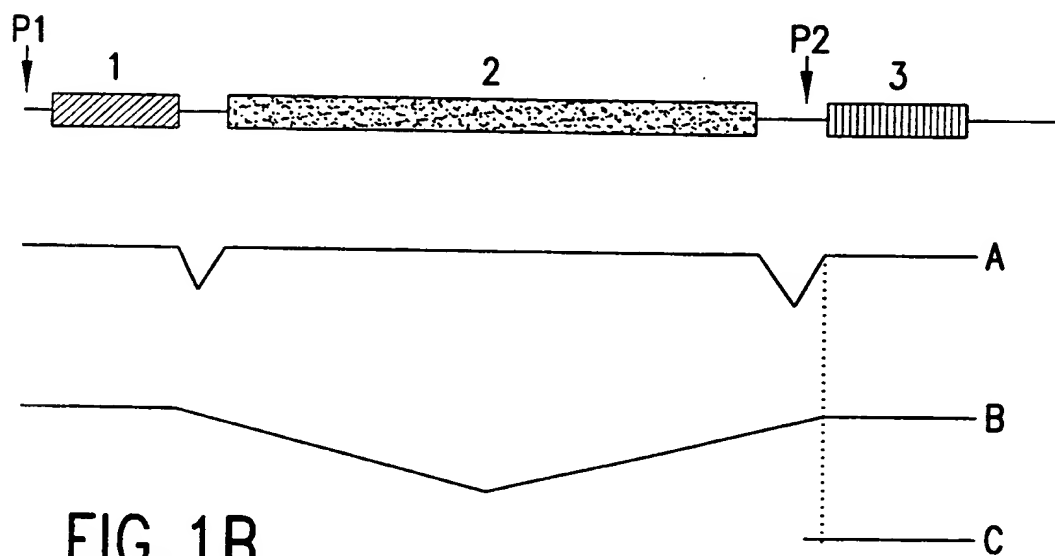


FIG. 1B

ATTG CTGGCTGGG CGCGCGCGG GCGTGGACG TGGACAGG GCGTGGAC ATCTGATCG
 CGAAGGAGG AGAAGCAGT TCATGTTCC GGGAGCGGTC GCTCTGCGG GTTCTTGGC TGGCTGGC AGCAGTGGC CTGCTGGC CTGCGGAGT
 TTGCCCCAACC CCCACAGG TGAAGAGAG CGCGCGGCTGG GGGCTGTAG CTGAGCATC GTGGCGGACC CGCCAGCC (ATG)GAAGACATA
 M E D I 4
 GACCAGTCT CGCTGGCTTC CTGCTGACG GACAGCGCGG CGCGCGCTTC AGTACAGT TCGTACCGA GCGCGAGGAC GAGGAGGAGG
 D Q S S L V S S S T D S P P R P P P A F K Y Q F V T E P E D E E D 37
 AGGAGGAGG GAGGAGGAGG AGGAGGAGG AGGAGGAGG GAGGAGGAGG AGGAGGAGG GAGGAGGAGG GAGGAGGAGG
 E E E E E D E D E D L E E L E V L E R K P A A G L S A A A V 70
 GCGCGCGCGG TCGTGGCTTC GAGGAGGAGG TGGTGGCGG CGCGCGCGG GCGCGCGCGG GCGCGCGCGG TCGTGGAGG
 P P A A A A P L L D F S S D S V P P A P R G P L P A A P P A A P E R 104
 GAGCATCTT GGAAGGAGG CGCGCGCGG CCGTGGCGG GCGTGGCGG GCGTGGCGG GCGTGGCGG GCGTGGCGG
 Q P S W E R S P A A P S L P P A A A V L P S K L P E D D E P P 137
 CGAGGCGCGG CGCTGGCGG CGAGCGCGG GCGCGCGG CCGTGGCGG GCGCGCGG GCGCGCGG GCGTGGCGG
 A R P P P P P A G A S P L A E P A A P S T P A A P K R R G S G 170
 AGTGGATGAG ACCCTTTTTC GCTCTGCGG TCGTGGAG CCGTGGAG CCGTGGAG AGAAGAAAT ATGATTTGA TGGAGGAGG AGTAAACAT
 S V D E T L F A L P A A S E P V I P S S A E K I M D L M E Q P G N T 204
 GTTCTGCTG GTCAGAGG TTTCCCATCT GCTCTGCTG AACTGCTG CCGTGGCGG GCGTGGCGG GCGTGGCGG GCGTGGCGG
 V S S G Q E D F P S V L L E T A A S L P S L S P L S T V [S] F K E H 237
 GATACCTGG TAACTTATCA GAGTGTGAT CCGTGGAGG AACTTGTAA GAACTTAA ATGAGCTTC TAAAGCTTC CCAGAGAGG CAACAATCC
 G Y L G N L S A V S S S E G T I E E T L N E A S K E L P E R A T N 270

FIG. 2A1

ATTGTAAT AGACATTTAG CAGAAATTTIC AGAATTAGAA TATTCAGAAA TGGGATCATC TTTTAAAGCC TCCCAAAAG GAGAGTCAGC CATATTAGTA
 P F V N R D L A E F S E L E Y S E M G S [S] F K G [S] P K G E S A I L V 304

 GAAACACTA AGGAAGAAGT AATTGTGAGG AGTAAGACA AAGAGGATTT AGTTGTAGT GCAGCCCTTC ACAGTCCACA AGAATCACCT GTGGTAAAG
 E N T K E E V I V R S K D K E D L V C S A A L H S P Q E S P V G K 337

 AAGACAGAGT TGTGCTCCA GAAAGACAA TGGACATTTT TAATGAAATG CAGATGTCAG TAGTAGCACC TGTGAGGAA GAGTATCCAG ACTTTAAGCC
 E D R V V S P E K T M D I F N E M Q M S V V A P V R E E Y A D F K 370

 ATTGAACAA GCATGCCAAG TGAAGATAC TATGAGCGA AGTAGCGATG TCGTGGCTGC TAGAGCTAAT GTGGAAGTA AAGTGACAG AAAATGCTTG
 P F E Q A W E V K D T Y E G S R D V L A A R A N V E S K V D R K C I 404

 GAAGATAGCC TGGAGCAAAA AAGTCTTGGG AAGCATAGTG AAGGCAGAAA TGAGGATGCT TCTTCCCA GTACCCCGA ACCGTGAAG GACAGCTCCA
 E D S L E Q K S L G K D S E G R N E D A S F P S T P E P V K D [S] S 437

 GACCATATAT TACCTGTGCT TCCTTTACCT CAGCAACCGA AAGCACCACA GCAACACAT TCCCTTGTGTT AGAAGATCAT ACTTCAGAAA ATAAACAGA
 R A Y I T C A S F T S A T E S T T A N T F P L L E D H T S E N K T 470

 TGAACAAAA ATACAGAAA GGAAGGCCCA AATTATAACA GAGAAGACTA GGCACAAAG GTCAATCTT TCCCTGTAG CAGTACAGGA TCTGAGGCA
 D E K K I E E R K A Q I I [T] E K T [S] P K T S N P F L V A V Q D S E A 504

 GATTATGTTA CAACAGATAC CTTATCAAG GTGACTGAGG CAGCAGTGT CAAACATGCC TGAAGTCTGA CCCCAGATTT AGTTCAGGAA GCAATGIGAAA
 D Y V T T D T L S K V T E A A V S N M P E G L T P D L V Q E A C E 537

 GTGAACAGAA TGAAGCCACA GGTACAAGA TTGCTTAIGA AACAAAGTG GACTGTGTC AACATCAGA AGCTATACAA GAATCACTTT ACCCCACAGC
 S E L N E A T G T K I A Y E T K V D L V Q T S E A I Q E S L Y P T 570

 ACAGCTTGGC CCATCATTTG AGGAAGCTGA AGCAACTCG TCACCAGTTT TCCCTGATAT TCGTATGAA GCACCATTA AATCTCTCTT TCCAAGCGCT
 A Q L C P S F E E A E A T P S P V L P D I V M E A P L N S L L P S A 604

FIG. 2A2

GGTGCCTCTG TAGTCAGCC CAGTGTATCC CCACTGGAG CACCTCCTCC AGTTAGTAT GACAGTATAA AGCTTGAGCC IGAAAACCCC CCACCATATG
G A S V V Q P S V S P L E A P P P V S Y D S I K L E P E N P P P Y 637

AAGAAGCCAT GAATGTAGCA CTAAAGCTT TGGGAACAAA GGAAGCAATA AAAGAGCTG AAAGTTTTAA TGCAGCTGT CAGGAACACAG AAGCTCTTA
E E A M N V A L K A L G T K E G I K E P E S F N A A V Q E T E A P 670

TATATCCATT GCGTGTGATT TAATTAAAGA AACAAAGCTC ICCACTGAGC CAAGTCAGA TTCTCTAAT TATTCAGAAA TAGCAAAATT CGAGAAGTCG
Y I S I A C D L I K E T K L S T E P S P D F S N Y S E I A K F E K S 704

GIGCCCGAAC AGCCTGAGCT AGTGGAGGAT TCCACACCTG AATCTGAACC AGTTGACTTA TTAGTGATG ATTCGATCC TGAAGTCCCA CAAACACAAG
V P E H A E L V E D S S P E S E P V D L F S D D S I P E V P Q T Q 737

AGGAGGCTGT GATGCTCATG AAGCAGAGTC TCACCTGAAGT GCTGAGACA GTAGCCAGC ACAAGAGGA GAGACTTAGT GCCTCACCCTC AGGAGCTAGG
E E A V M L M K E S L T E V S E T V A Q H K E E R L S A S P Q E L 770

AAGCCATAT TTAGAGTCTT TTCAGCCCAA TTTACATAGT ACAAGAGATG CTGCATCTAA TGACATTCCTA ACATTCACCA AAAGGAGAA AATTCCTTIG
G K P Y L E S F Q P N L H S T K D A A S N D I P T L T K K E K I S L 804

CAAATGGAAG AGTTTAATAC TCAATTTAT TCAATGATG ACTTACTTC TTCTAAGAA GACAAAATAA AAGAAAGTGA AACATTTTCA GATTCATCTC
Q M E E F N T A I Y S N D D L L S S K E D K I K E S E T F S D S S 837

CGATTGAGAT AATAGATGAA TTTCACAGCT TTGTCAGTGC TAAAGATGAT TCTCTAAAT TAGCCAAGCA GTACACIGAT CTAGAAGTAT CCGACAAAAG
P I E I I D E F P T F V S A K D D S P K L A K E Y T D L E V S D K 870

TGAAATTCCT AATATCCAAA GCGGGGCGAGA TTCAATTCCTT TCGTTAGAAT TGCCCTGTGA CCTTCTTTC AGAATATAT ATCCTAAAGA TGAAGTACAT
S E I A N I Q S G A D S L P C L E L P C D L S F K N I Y P K D E V H 904

GTTCACAGAT AATTCCTCGA AAATAGGCTCC AGCTGATCTA AGGCATCCAT ATCCCTCTCA AATGCTCTG CTITGGAAAC TCAGACAGAA ATGGGCACCA
V S D E F S E N R S S V S K A S I S P S N V S A L E P Q T E M G S 937

FIG. 2A3

TAGTAAATC CAAATCATT ACCAAAGAAG CAGAGAAAAA ACTTCTTCTI GACACAGAGA AAGAGGACAG ATCCCTGTCA GCTGTATTGT CAGCAGAGCT
I V K S K S L T K E A E K K L P S D T E K E D R S L S A V L S A E 970

GAGTAAACT ICAGTGTGTG ACCTCTCTTA CTGGAGAGAC ATTAGAAGA CTGGAGTGGT GTTGTGGTCC AGCTTATICC TGTGCTGCTG ICIGACAGTIG
L S K T S V V D L L Y W R D I K K T G V V F G A S L F L L L S L T V 1004

TTCCGATTG TCAGTGTAC GGCCTACATT GCCTTGGCCC TGTCTCGGT GACTATCAGC TTTAGGATAT ATAAGGCGT GATCCAGCT ATCCAGAAAT
F S I V S V T A Y I A L A L L S V T I S F R I Y K G V I Q A I Q K 1037

CAGATGAAG CCACCCATTC AGGCATATT TAGAATCTGA AGTGTCTATA TCAGAGCAAT TGGTTCAGAA ATACAGTAAT TGTGCTGTG GTCATGTGAA
S D E G H P F R A Y L E S E V A I S E E L V Q K Y S N S A L G H V 1070

CAGACAATA AAAGAACTGA GGGGGCTTTT CTAGTGTAT GATTAGTGT ATTCCTGAA GTTGTGAGTG TTGATGTTGG TGTIATCTTA TGTGTGCTCC
N S T I K E L R R L F L V D D L V D S L K F A V L M W V F T Y V G A 1104

TGTGTCAATG GTCTGACACT ACTGATTTTA GCCTGTGATC CACTCTTCAG TATCTCTGT ATTATGAC GGCATCAGT GCAGATAGAT CATTAICTAG
L F N G L T L L I L A L I S L F S I P V I Y E R H Q V Q I D H Y L 1137

GACTTGCAA CAAGAGTGT AAGGATGCCA TGGCCAAAT CCAAGCAAA ATCCCTGGAT TGAAGCCAA AGCAGATTGA AAAAGCCCCA AACAGAGT
G L A N K S V K D A M A K I Q A K I P G L K R K A D * 1163

CATCTTTAA GGGGACACT ACTGATTAC GGGGTGGGA GGGTCAGGG TGAAGCCCTTG GTGGCGTGC GTTTCAGCT CTTTATTTT AGCAGTGCAC
TGTGTGAGGA AAATTAACCT GTCTGACTT CCTGTGTTA TCATCTAAG TATGTAAAG TGTGTGTAT GGATCTCAT TTGCTTCC
CAATGAGCG CCTGGTGAAT AAAGGACTCG GGGAAAGCIG TGCATGTAT CTGCTGAGG GTAGTACG TGTATGAGA GAGTGTAA GAAGGCAAT
CTGGGGCCAG GGAACCCCT TTTACAGTG TACTGTGTT GTTCAGTGA AAAGTATGC AGATTTTCT GAAATGAAAT GTTATGATGA GAGCATACTA
CTAAAGCAGA GTGGAACACT CTGCTTTAT GGCTGTCTI AGGCTATIG TGAATTTACT GTTATATGC CAATATACT AAATATAGAC CTAATCTATA
TATAGTGT CACAAGCTT AGATCTTTAA CCTTGCAGT CCCCCACAGT GCCTGACCTC TGAGTCAATG GTTATGAGT GTAGTCCCA GCACATAAC
TAGGAAGAGA AATGTATTG TAGGAGTCT ACCTACCACC TGTTTTCAAG AAAATATAGA ACTCCAACA AAATATAGAA TGICATTICA AAGACTTACT
GTATGTATAG TTAATTTGT CACAGACTCT GAAATCTAT GAGCTTCTC AAATGTTGC AGTATCAAA CATTTGTTATG CAAGAAATCA
TAAATGAG ACITATACCA TTGTGTTTA AGCGTACTG AATTATCTGT GGAATGCAIT GTGAAGTGA AAGCAAACT ATCAATAAG CTTATAGACT
TAAAAAAA AAAAAAAA

FIG. 2A4

peptide 1:	EYLGDLPAVLPT	peptide 4:	KXFEXVWEV
(bovine)	EYLGDLPAVLPT	(bovine)	KPFERVWEV
(rat)	gYLGnLsAVsssE	(rat)	KPFEQaWEV
peptide 2:	EIAEIQDG ESL	peptide 5:	VVDLLYWRDIK
(bovine)	EIAAdIQDGagSL	(bovine)	VVDLLYWRDIK
(rat)	EIAAnIQsGadSL	(rat)	VVDLLYWRDIK
peptide 3:	KXYLESIQPSLGITK	peptide 6:	KAVAAEASMREEYADF
(bovine)	KPYLESfQPSLGITK	(bovine)	KgVAAEASMGEEYADF
(rat)	KPYLESfQPnLhsTK	(rat)	mqmsvvApvREEYADF

FIG.2B

TABLE 2260000

CHS-REX	1	NLLYWRDIKQ	TGIVFGS	LL	LLFSLTQF	SV	VS	VAYLALA	GL	SATISFRI	50
U51048	1	NLLWRNSRK	TIVFTGILL	LL	LDVMHVS	SV	SV	SMVGIT	VL	IAGHRL	50
NOGOBOV	1	DLLTWRDIKQ	TGIVFGS	LL	LLFSLTQF	SV	SV	SMVGIT	VL	IAGHRL	50
NOGORAT	1	DLLYWRDIKQ	TGIVFGS	LL	LLFSLTQF	SV	SV	SMVGIT	VL	IAGHRL	50
NSP	1	DLLYWRDIKQ	TGIVFGS	LL	LLFSLTQF	SV	SV	SMVGIT	VL	IAGHRL	50
S-REX	1	DLLYWRDIKQ	TGIVFGS	LL	LLFSLTQF	SV	SV	SMVGIT	VL	IAGHRL	50
W06A7A	1	DVLYWRDAKK	SAILVSLAL	LL	LLFSLTQF	SV	SV	SMVGIT	VL	IAGHRL	50
CHS-REX	51	YKSVLQAMQK	TDEGHPFKAY	LD	MEMLSQD	QI	QI	QYTDCLQ	LY	VNSTVKEL	100
U51048	51	LVQFWSIWKK	DENKQILRF	Y	PHKIEIPR	EET	LY	LAGKA	VSHIN	ILNR	100
NOGOBOV	51	YKGVIIQAIQK	SDEGHPFRAY	LE	SEVAISEE	LV	QKYSNSAL	CHVNC	TIKEL		100
NOGORAT	51	YKGVIIQAIQK	SDEGHPFRAY	LE	SEVAISEE	LV	QKYSNSAL	CHVNC	TIKEL		100
NSP	51	YKSVLQAMQK	TDEGHPFRAY	LE	SEVAISEE	LV	QKYSNSAL	CHVNC	TIKEL		100
S-REX	51	YKSVLQAMQK	TDEGHPFRAY	LE	SEVAISEE	LV	QKYSNSAL	CHVNC	TIKEL		100
W06A7A	51	FKKVEAQIKK	TDSEHPFSEI	LA	QDLTPQE	KV	HAQADVFV	E	HATCIANKL		100
CHS-REX	101	RRLFLVQDLV	DSLKF	AVLMW	LL	TYVGALFN	GL	TLLIMAMV	SMF	TL	PPVVD
U51048	101	MIELLVEKW	EDSLKFLVLL	CG	INLLGDCF	NGL	TLLIFGM	CICCLTLLYL			
NOGOBOV	101	RRLFLVDDL	DSLKF	AVLMW	VFTY	VGALFN	GL	TLLILAL	SL	FSVPV	IYE
NOGORAT	101	RRLFLVDDL	DSLKF	AVLMW	VFTY	VGALFN	GL	TLLILAL	SL	FSVPV	IYE
NSP	101	RRLFLVDDL	DSLKF	AVLMW	LL	TYVGALFN	GL	TLLIMAMV	SMF	TL	PPVVD
S-REX	101	RRLFLVDDL	DSLKF	AVLMW	LL	TYVGALFN	GL	TLLIMAMV	SMF	TL	PPVVD
W06A7A	101	KKLVEFESPL	ESIKFGLVLM	SL	TYIASWFS	GF	TLLILGLL	GVF	SV	PKVYE	200
CHS-REX	151	KYQAQIDQYL	GLVRTHINTV	VAKI	QAKIPG	AK					
U51048	151										
NOGOBOV	151	RHQQAQIDHYL	GLANKNVKDA	MAKI	QAKIPG	LK					
NOGORAT	151	RHQQAQIDHYL	GLANKSVKDA	MAKI	QAKIPG	LK					
NSP	151	KHQQAQIDQYL	GLVRTHINAV	VAKI	QAKIPG	AK					
S-REX	151	KHQQAQIDQYL	GLVRTHINTV	VAKI	QAKIPG	AK					
W06A7A	151	SNQEAIDPHL	ATISGHLKNV	QNI	IDEKIPF	LR	SAPVAEE				

FIG. 3A

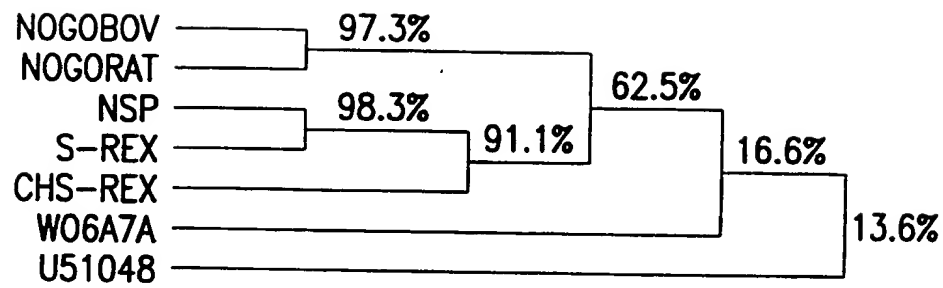


FIG. 3B

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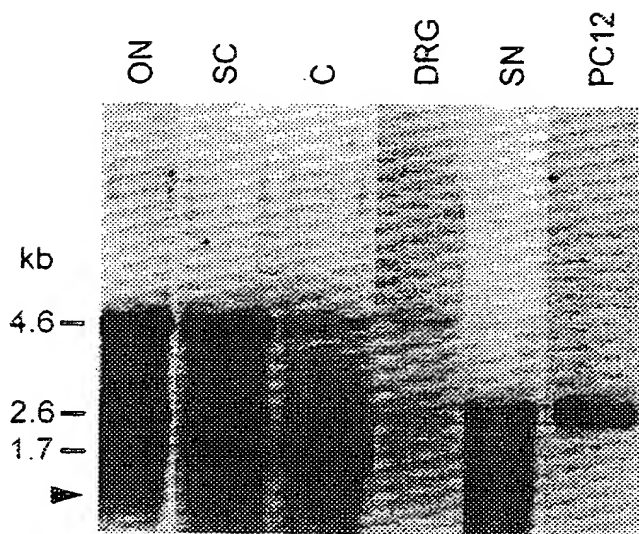


FIG.4A

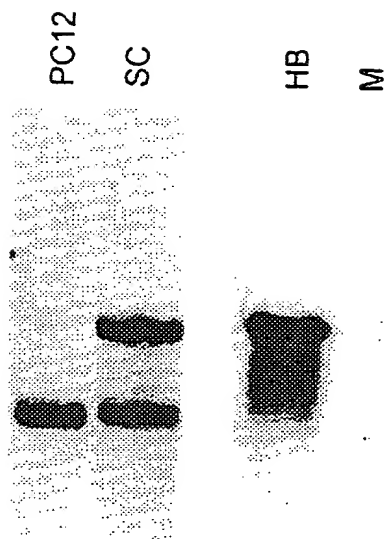


FIG.4B

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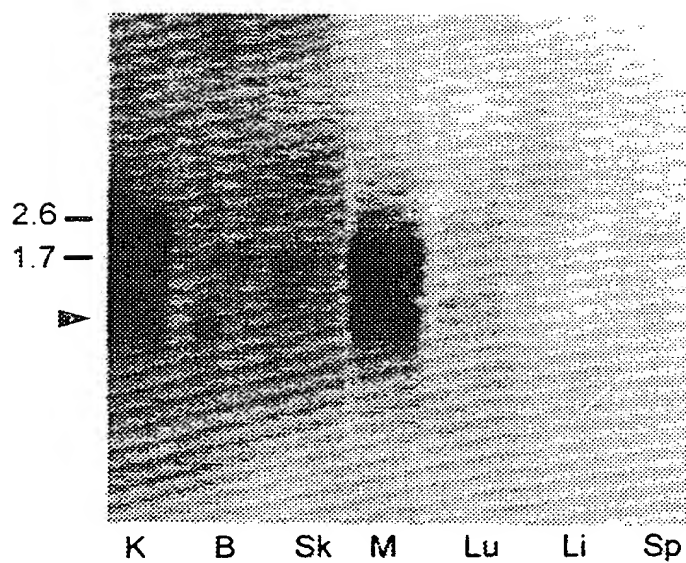


FIG.4C

FIG. 5A

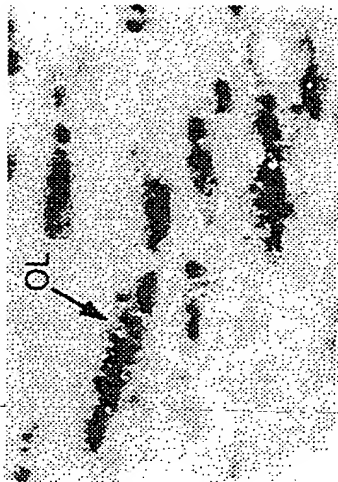


FIG. 5B

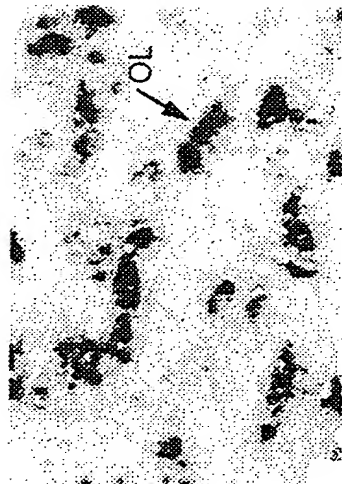


FIG. 5C

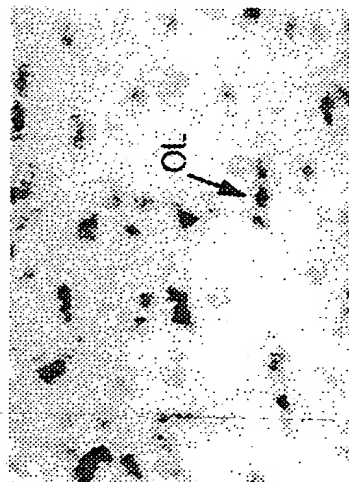
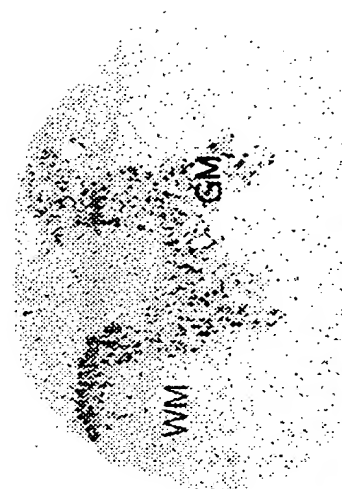


FIG. 5D

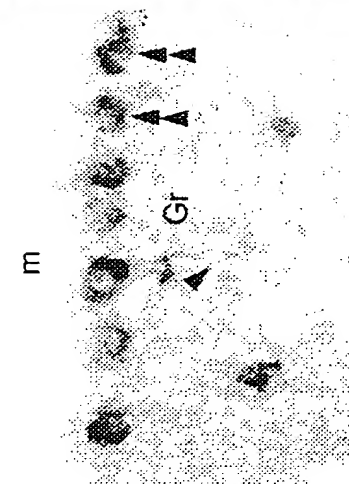


FIG. 5E



FIG. 5F

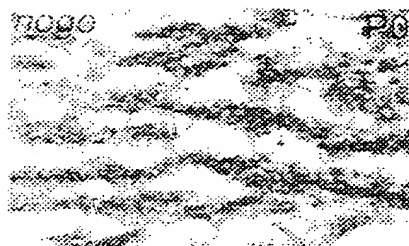


FIG. 6A



FIG. 6B

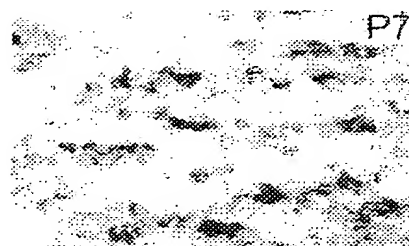


FIG. 6C



FIG. 6D

plp P3

FIG. 6G



FIG. 61

1. The first part of the document is a list of names and their corresponding addresses. The names are listed in a column on the left, and the addresses are listed in a column on the right. The names are: John A. Smith, John B. Smith, John C. Smith, John D. Smith, John E. Smith, John F. Smith, John G. Smith, John H. Smith, John I. Smith, John J. Smith, John K. Smith, John L. Smith, John M. Smith, John N. Smith, John O. Smith, John P. Smith, John Q. Smith, John R. Smith, John S. Smith, John T. Smith, John U. Smith, John V. Smith, John W. Smith, John X. Smith, John Y. Smith, John Z. Smith. The addresses are: 123 Main St., 456 Main St., 789 Main St., 101 Main St., 202 Main St., 303 Main St., 404 Main St., 505 Main St., 606 Main St., 707 Main St., 808 Main St., 909 Main St., 1010 Main St., 1111 Main St., 1212 Main St., 1313 Main St., 1414 Main St., 1515 Main St., 1616 Main St., 1717 Main St., 1818 Main St., 1919 Main St., 2020 Main St., 2121 Main St., 2222 Main St., 2323 Main St., 2424 Main St., 2525 Main St., 2626 Main St., 2727 Main St., 2828 Main St., 2929 Main St., 3030 Main St., 3131 Main St., 3232 Main St., 3333 Main St., 3434 Main St., 3535 Main St., 3636 Main St., 3737 Main St., 3838 Main St., 3939 Main St., 4040 Main St., 4141 Main St., 4242 Main St., 4343 Main St., 4444 Main St., 4545 Main St., 4646 Main St., 4747 Main St., 4848 Main St., 4949 Main St., 5050 Main St., 5151 Main St., 5252 Main St., 5353 Main St., 5454 Main St., 5555 Main St., 5656 Main St., 5757 Main St., 5858 Main St., 5959 Main St., 6060 Main St., 6161 Main St., 6262 Main St., 6363 Main St., 6464 Main St., 6565 Main St., 6666 Main St., 6767 Main St., 6868 Main St., 6969 Main St., 7070 Main St., 7171 Main St., 7272 Main St., 7373 Main St., 7474 Main St., 7575 Main St., 7676 Main St., 7777 Main St., 7878 Main St., 7979 Main St., 8080 Main St., 8181 Main St., 8282 Main St., 8383 Main St., 8484 Main St., 8585 Main St., 8686 Main St., 8787 Main St., 8888 Main St., 8989 Main St., 9090 Main St., 9191 Main St., 9292 Main St., 9393 Main St., 9494 Main St., 9595 Main St., 9696 Main St., 9797 Main St., 9898 Main St., 9999 Main St.

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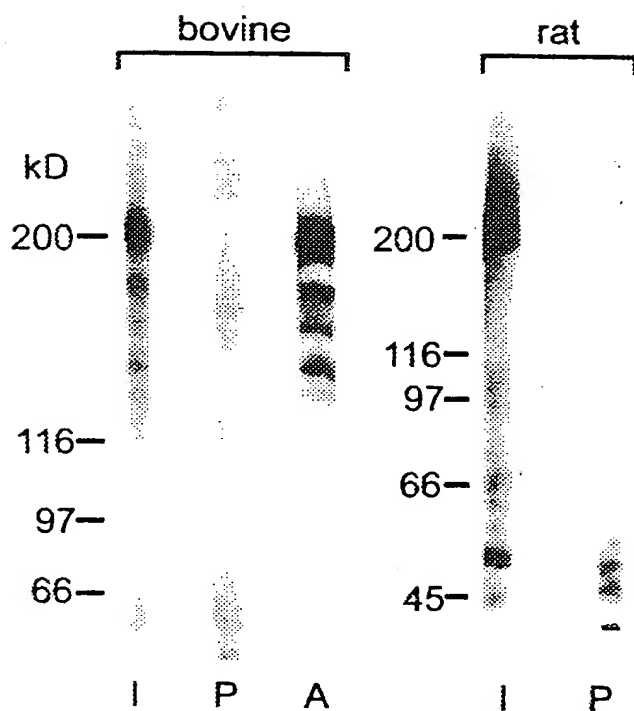


FIG.7A

FIG.7B

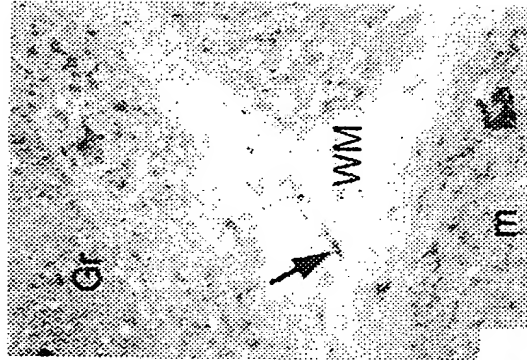
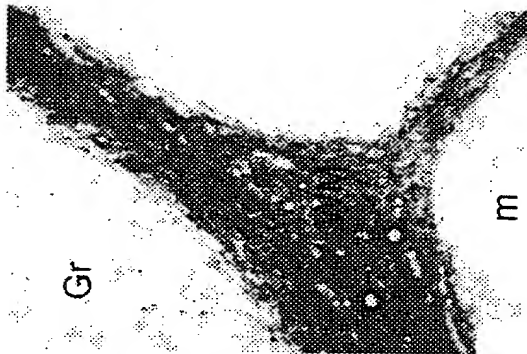


FIG. 8C



F.G.B.

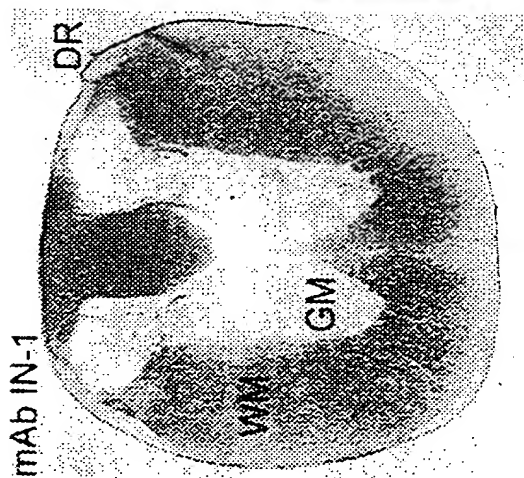


FIG. 8A

FIG. 8D

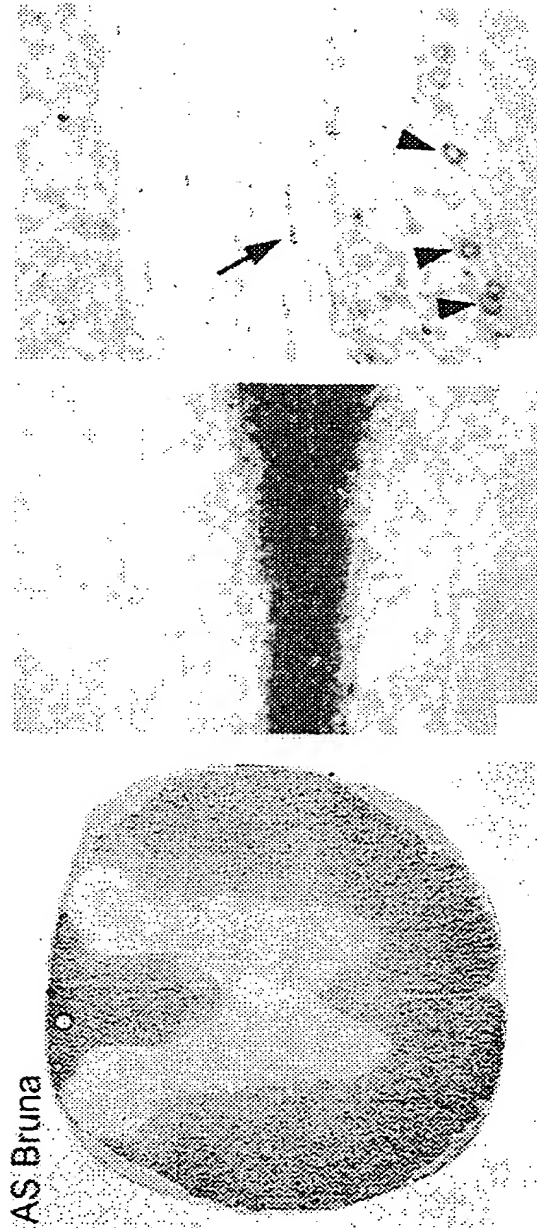


FIG. 8F

FIG. 8E

FIG. 8D

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FIG. 8G



FIG. 8G



FIG. 8H



FIG. 8I

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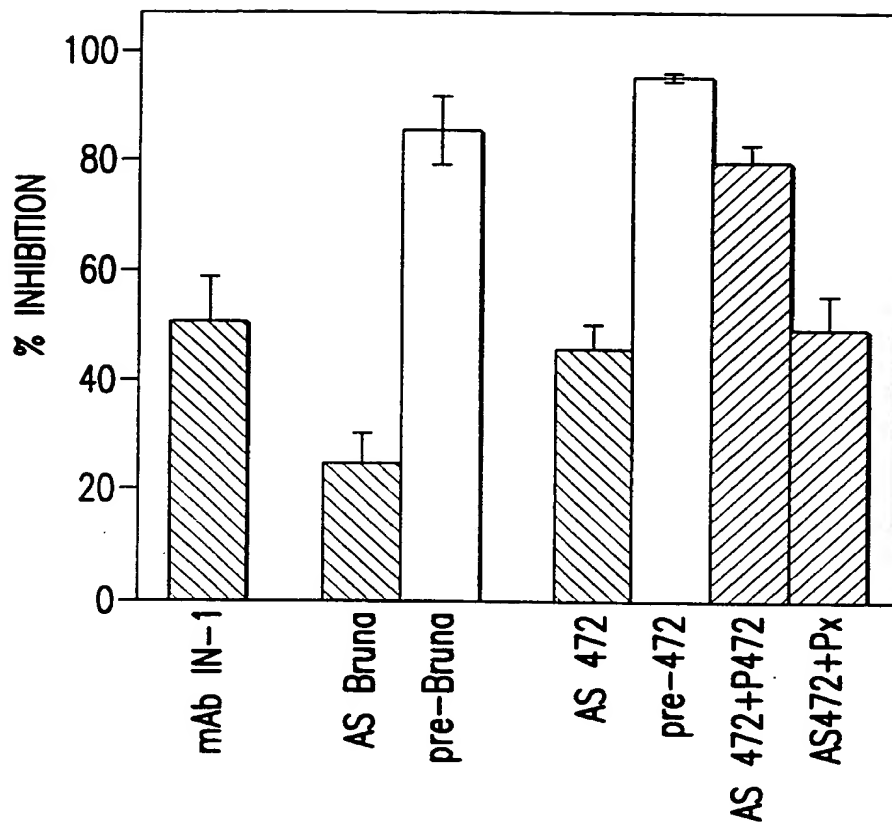


FIG.9A

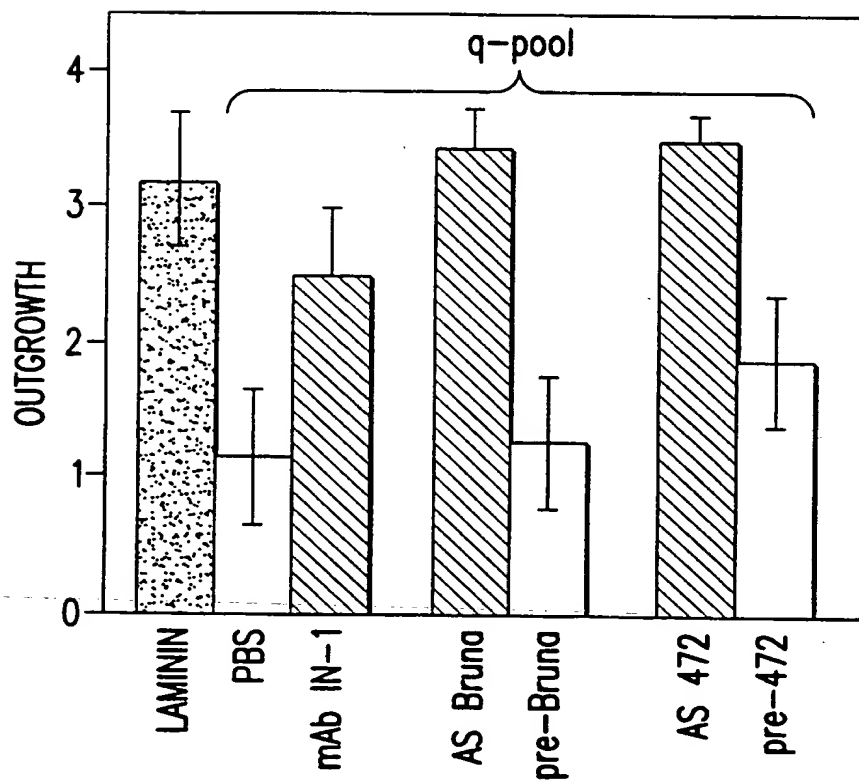


FIG.9B

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T04260" 2260E960

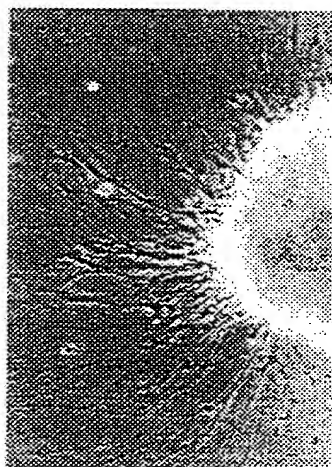


FIG.9D

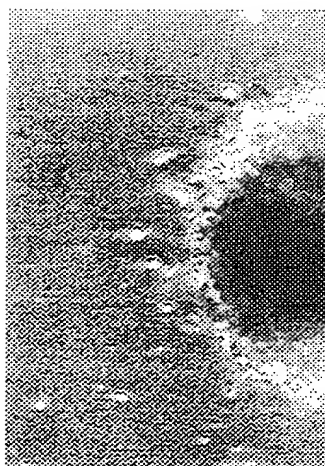


FIG.9C

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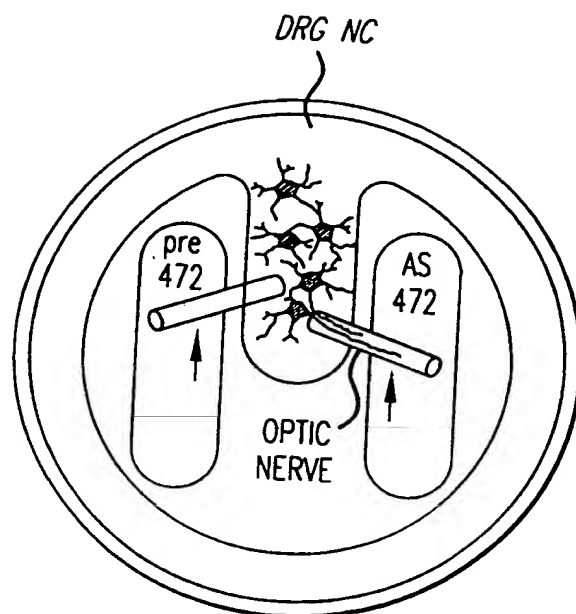


FIG.10A

CULTURE	pre-472	AS 472
1	-	++
2	-	+++
3	+	+++
4	+	-
5	-	+++
6	+	+++
7	++	++
8	+	++
9	+	++
10	-	+++

AXONS/NERVE: - = 0; + = 1-20; ++ = 20-50; +++ = 50->300

FIG.10B

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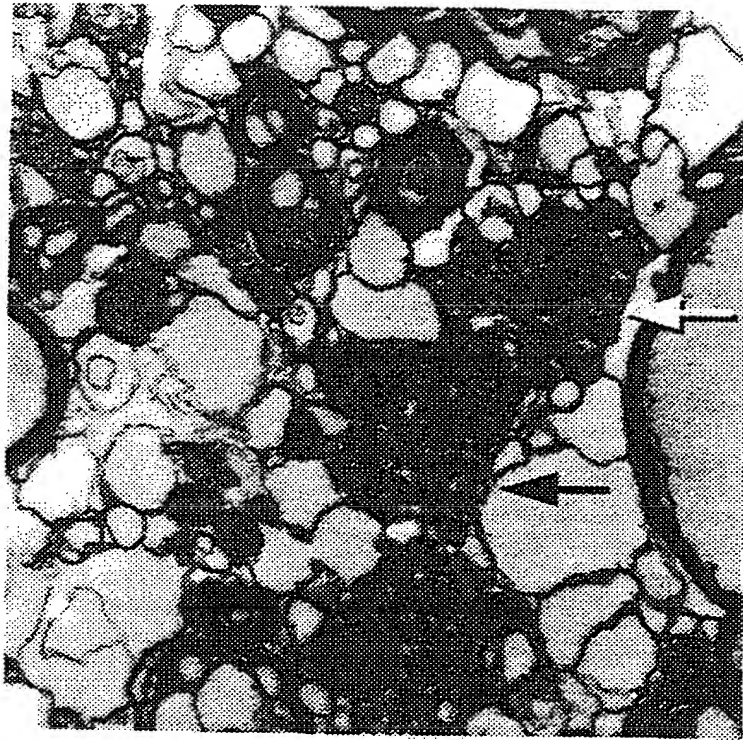


FIG. 10C



FIG. 10D

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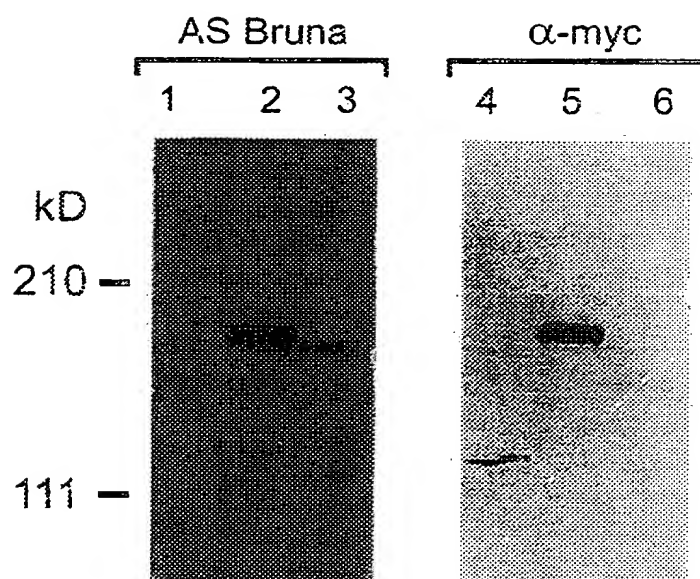


FIG.11A

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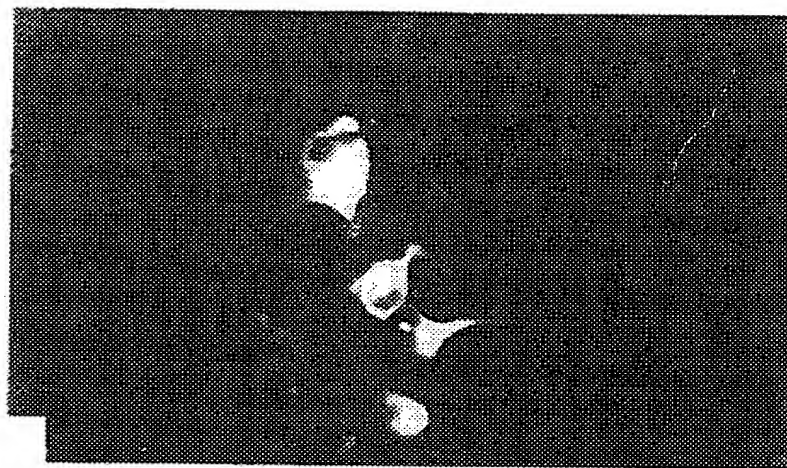


FIG. 11B

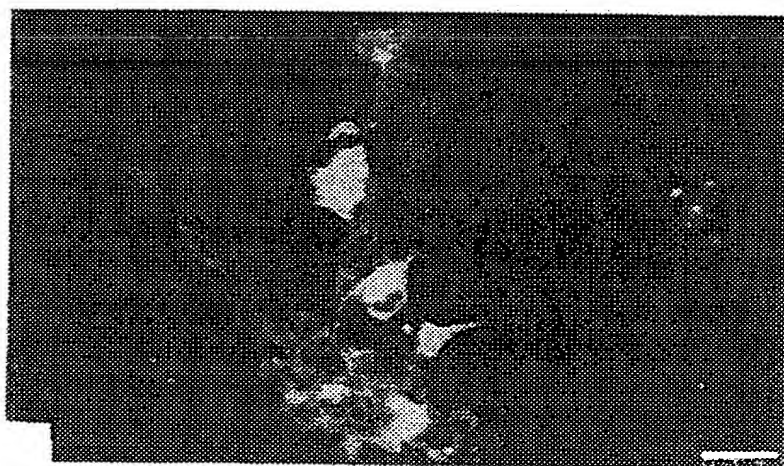


FIG. 11C

09830972.092401

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10	20	30	40	50	60
CTATCTCCTC	TCTCAGCCGC	TGCTTTTAAA	GAACGTGAAT	ACCTTGGTGA	TTTACCAGCA
70	80	90	100	110	120
GTACTGCCCA	CTGAAGGAAC	ACTTCCAGCA	ACTTCAAATG	AAGCTTCTAA	AGCATTCTCA
130	140	150	160	170	180
GAGAAGGCAA	AAAATCCATT	TGTAGAGAGA	AATTTAACAG	AATTTTCAGA	ATTGGAATAT
190	200	210	220	230	240
TCAGAAATGG	AATCATCATT	CAGTGGCTCT	CAAAAGGCAG	AACCTGCCGT	AACAGTAGCG
250	260	270	280	290	300
AATCCTAGGG	ACGAAATAGT	TGTGAGGAGT	AGAGATAAAG	AAGAGGACTT	AGTTAGTCTT
310	320	330	340	350	360
AACATCCTTC	ATACTCAGCA	GGAGTTATCT	ACAGTCCTTA	CGAAATCAGT	TGAAGAAGAA
370	380	390	400	410	420
GATAGAGTTC	TGTCTCCAGA	AAAAACAAAG	GACAGTTTTA	AGGAAAAGGG	AGTTGCAGCA
430	440	450	460	470	480
GAAGCTTCTA	TGGGGGAGGA	ATATGCAGAC	TTCAAACCAT	TTGAGCGAGT	ATGGGAAGTG
490	500	510	520	530	540
AAAGATACTT	ACAAGCAAGA	TAGTGATGTT	TTGATTGCTG	GAGGTAATAT	AGAGAGCAAA
550	560	570	580	590	600
TTGGAAGGTA	AAGTGGATAA	GAAACACTTT	TCAGATAGCC	TTGAACAAAC	AAATCGTGAA
610	620	630	640	650	660
AAAGATAGTG	AAAGCAGTAA	TGATGACACT	TCATTTCCCA	GTACACCAGA	AGCTGTAAGA
670	680	690	700	710	720
GGTGGTTCCG	GAGCGTACAT	CACGTGTGCT	CCCTTTAACC	CAACAACTGA	GAATGTTTCA
730	740	750	760	770	780
ACAAACATTT	TTCCCTTGTT	GGAAGATCAT	ACTTCGGAAA	ATAAGACAGA	TGAAAAAAAG
790	800	810	820	830	840
ATAGAAAAAA	AAAGGCACAA	ATTGTAACAG	AGAAGAATGC	AAGTGTCAAG	ACATCAAACC
850	860	870	880	890	900
CTTTCCTTAT	GGCAGCACAG	GAGTCTAAGA	CAGATTACGT	TACAACAGAT	CATGTGTCAA
910	920	930	940	950	960
AGGTGACCGA	GGAAGTAGTG	GCAAACATGC	CTGAAGGTCT	AACCCACAGT	TTGGTTCAGG
970	980	990	1000	1010	1020
AAGCATGTGA	AAGTGAATTG	AATGAAGCTA	CTGGTACAAA	AATTGCCTTT	GAAACAAAAA
1030	1040	1050	1060	1070	1080
TGGACCTGGT	TCAAACCTCA	GAAGCTGTGC	AGGAGTCACT	TTACCCTGTA	ACACAGCTTT
1090	1100	1110	1120	1130	1140
GCCCATCTTT	TGAAGAATCT	GAAGCTACTC	CGTCACCGGT	TTGCCTGAC	ATTGTCATGG
1150	1160	1170	1180	1190	1200
AAGCACCATT	AAATTCTGTA	GTTCTAGTGT	CTGGTGCTTC	TGCAGTGCAG	CTCAGTTCAT
1210	1220	1230	1240	1250	1260

FIG 12A

SUBSTITUTE SHEET (RULE 26)

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CACCATTAGA AACTCTTCCT TCAGTTAATT ATGAAAGCAT AAAGTTTGAG CCTGAAAATC
 1270 1280 1290 1300 1310 1320
 CCCCACCATA TGAGGAGGCC ATGAATGTAT CACTAAAAAA AGAATCAGGA ATGAATGAAG
 1330 1340 1350 1360 1370 1380
 AAATCACAGA GCCTGAAGGT ATTAGTGTAG CTGTTTCAGGA AACAGAAGCT CCTTATATAT
 1390 1400 1410 1420 1430 1440
 CTATTGCATG TGATTTAATT AAAGAAACAA AGATCTCTAC TGAACCGACT CCAGATTTCCT
 1450 1460 1470 1480 1490 1500
 CTAGTTATTC AGAAATAGCA GAAGTTGCAC AGCCAGTGCC CGAGCATTCT GAGCTAGTTG
 1510 1520 1530 1540 1550 1560
 AAGATTCTC CCCCATTCT GAACCAAGTTG ACTTATTTAG TGATGATTCA ATACCCGAAG
 1570 1580 1590 1600 1610 1620
 TTCCACAAAA ACAAGATGAA GCTGTAATAC TTGTGAAAGA AACCTCACT GAAATTTTCAT
 1630 1640 1650 1660 1670 1680
 CTGAGTCAAT GACAGGACAT GACAATAAGG GAAAACTCAG TGCTTCACCA TCACCTGAGG
 1690 1700 1710 1720 1730 1740
 GAGGAAAACC GTATTGGAG TCTTTTCAGC CCAGTTTAGG CATCACAAAA GATACCTTAG
 1750 1760 1770 1780 1790 1800
 CACCTGATGA AGTTTCAGCA TTGACCCAAA AGGAGAAAAT CCCTTTGCAG ATGGAGGAGC
 1810 1820 1830 1840 1850 1860
 TCAATACTGC AGTTTATTCA AGTGATGGCT TATTCATTGC TCAGGAAGCA AACCTAAGAG
 1870 1880 1890 1900 1910 1920
 AAAGTGAAC ATTTTCAGAT TCATCTCCGA TTGAGATTAT AGATGAGTTC CCGACCTTTG
 1930 1940 1950 1960 1970 1980
 TCAGTTCTAA AGCAGATTCT TCTCCTACAT TAGCCAGGGA ATACACTGAC CTAGAAGTAG
 1990 2000 2010 2020 2030 2040
 CCCACAAAAG TGAAATTGCT GACATCCAGG ATGGAGCTGG GTCATTGGCT TGTGCAGGAT
 2050 2060 2070 2080 2090 2100
 TGCCCCATGA CCTTTCTTTC AAGAGTATAC AACCTAAAGA GGAAGTTCAT GTCCCAGATG
 2110 2120 2130 2140 2150 2160
 AGTTCTCCAA AGATAGGGGT GATGTTTCAA AGGTGCCCGT ACTGCCCTCCA GATGTTTCTG
 2170 2180 2190 2200 2210 2220
 CTTTGGATGC TCAAGCAGAG ATAGGCAGCA TAGAAAAACC CAAAGTTCTT GTGAAAGAAG
 2230 2240 2250 2260 2270 2280
 CCGAGAGAAA ACTTCCTTCT GATACAGAAA AAGAGCGAAG ATCTCCATCT GCTATATTTT
 2290 2300 2310 2320 2330 2340
 CAGCAGAGCT GAGTAAACT TCAGTTGTTG ACCTCCTCTA CTGGAGAGAC ATTAAGAAGA
 2350 2360 2370 2380 2390 2400
 CTGGAGTGGT GTTTGGTGCC AGCTTGTTCC TGCTGCTCTC GCTGACAGTA TTCAGCATTG
 2410 2420 2430 2440 2450 2460

FIG. 12B

SUBSTITUTE SHEET (RULE 26)

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TGAGTGAAC	GGCCTACATT	GCCTTGGCCC	TGCTCTCTGT	GACTATCAGC	TTTAGGATAT
2470	2480	2490	2500	2510	2520
ATAAGGGTGT	GATCCAGGCT	ATCCAGAAAT	CTGATGAAGG	CCACCCATTC	AGGGCATATT
2530	2540	2550	2560	2570	2580
TGGAATCTGA	AGTTGCTATA	TCTGAGGAGT	TGGTTCAGAA	GTACAGCAAT	TCTGCTCTTG
2590	2600	2610	2620	2630	2640
GTCATGTTAA	CTGCACAATA	AAAGAACTCA	GACGCCTCTT	CITAGTTGAT	GATTTAGTTG
2650	2660	2670	2680	2690	2700
ATTCTCTGAA	GTTTGCAGTG	TTGATGTGGG	TATTTACCTA	TGTTGGTGCC	TTGTTCAATG
2710	2720	2730	2740	2750	2760
GTCTGACACT	ACTAATTTTG	GCTCTGATTT	CACTCTTCAG	TGTTCTGT	ATTTATGAAC
2770	2780	2790	2800	2810	2820
GGCATCAGGC	GCAAATAGAT	CATTATCTGG	GACTTGCAAA	TAAGAATGTT	AAAGATGCTA
2830	2840	2850	2860	2870	2880
TGGCTAAAAT	CCAAGCAAAA	ATCCCTGGAT	TGAAGCGTAA	AGCTGAATGA	GAAAGCCTGA
2890	2900	2910	2920	2930	2940
AAGAGTTAAC	AATAGAGGAG	TTTATCTTTA	AAGGGGATAT	TCATTTGATT	CCATTGGGGA
2950	2960	2970	2980	2990	3000
GGGTCAGGGA	AGAACAAAGC	CTTGACATTG	CAGTGCAGTT	TCACAGATCT	TTATTTTATG
3010	3020	3030	3040	3050	3060
CAACGCAGTG	TCTGAGGAAA	AATGACCTGT	CTTGACTGCC	CTGTGTTTAT	CATCTTAAGT
3070	3080	3090	3100	3110	3120
ATTGTAAGCT	GCTATGTATG	GATTAAATC	GTAATCATAT	TTGTTTTTCC	TGTATGAGGC
3130	3140	3150	3160	3170	3180
ACTGGTGAAT	AAACAAAGAT	CTGAGAAAGC	TGTATATTAC	ACTTTGTCGC	AGGTAGTCTT
3190	3200	3210	3220	3230	3240
GCTGTATTTG	GGGAATTGCA	AAGAAAGTGG	AGCTGACAGA	AATAACCTTT	TTCACAGTTT
3250	3260	3270	3280	3290	3300
GTGCACTGTG	TACGGTCTGT	GTAGGTTGAT	GCAGATTTTC	TGAAATGAAA	TGTTTAGACG
3310	3320	3330	3340	3350	3360
AGATCATGCC	ACCAAGGCAG	GAGTGAAAAA	GCTTGCCTTT	CCTGGTATGT	TCTAGGTGTA
3370	3380	3390	3400	3410	3420
TTGTGAAATT	TACTGTTGTA	TTAATTGCCA	ATATAAGTAA	ATATAGATTA	TATATATCTA
3430	3440	3450	3460	3470	3480
TATATAGTGT	TTCACGAAGC	TTAGCCCTTT	ACCTTCCCAG	CTGCCCCACA	GTGCTTGATA
3490	3500	3510	3520	3530	3540
CTTCTGTCAT	GGGTTTTATG	TGTGTAGTCC	CAAAGCACAT	AAGCTAGGGA	GAAACGTACT
3550	3560	3570	3580	3590	3600
TCTAGGCGCA	CTACCATCTG	TTTTCAACAC	GAACCGACGC	CATGCAAACA	GAACCTCTCA
3610	3620	3630	3640	3650	3660
ACATAAACTT	CACTGCACAG	ACTTACTGTA	GTAAATTTTA	TCACAAACTC	TGGACTGAAT
3670	3680	3690	3700	3710	3720

FIG. 12C

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CTAATGCTTC CAAAAATGTT TGCAAATATC AAACATTGTT ATGTAAGAAA ATATAAATGA
3730 3740 3750 3760 3770 3780
CGATTATAC AATTGTGTT TAAGCTGTAT TGAACATAAT CTGTGGAATG CATTGTGAAC
3790 3800 3810 3820 3830 3840
TGTAAGCA AAGTATCAAT AAAGCTTATA GACTTAAAAA AAAAAAAAAA AAA.....

FIG. 12D

PCT/US99/26160

1	MEDLDQSPVLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEE-EEEDEDE	50
1	MEDIDQSSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEED-DE	50
51	DLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAA	100
51	DLEELEVLERKPAAGLSAAAVPPA-AA-APLLDFSSDSVPPAPRGPLPAA	100
101	PPVAPERQPSWDPSPVSSTVPAPSPLS-AAAVSPSKLPEDDEPPARPPPP	150
101	PPAAPERQPSWERSPAA--PAPS-LPPAAVLPSKLPEDDEPPARPPPP	150
151	PPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGS-SG----AV-----	200
151	PPAGASPLAEP-----A-AP--P-STPAAPKRRGSGSVDETLFALPAASE	200
201	-VXXXX--KIMDLKEQPGNTISAGQEDFPSVLLETAASXPSSLPLSAASF	250
201	PVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASXPSSLPLSTVSF	250
251	KEHEYLGNLSTVLPTEGTLQE--NVSEASKEVSEKAKTLLID-RDLTEFS	300
251	KEHGYLGNLSAVSSSEGTTIETLN--EASKELPERA-TNPFVNRDLAEFS	300
301	ELEYSEMGSSFSVSPKAESAVI-VANPREEIIVKNKDEEEKLV-SNNILH	350
301	ELEYSEMGSSFKGSPKGESA-ILVENTKEEVIVRSKDKED-LVCSAA-LH	350
351	XQQELPTALTKLV-KEDEVVSSEKAKDSFNEKR--VAVEAPMREEYADFK	400
351	SPQESP-----VGKEDRVVSPEKTMDFNEMQMSV-V-APVREEYADFK	400
401	PFERVWEVKDSKEDS-DMLAAGGKIESNLESKVDDKKCFADSLEQTNHEKD	450
401	PFEQAWEVKDTYEGSRDVLAAAR---NVESKVDRKCLEDSEQKSLGKD	450
451	SESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT-NIFPLLEDP	500
451	SEGRNEDASFPSTPEPVKDSSRAYITCASFTSA-TEST-TANTFPLLEDH	500
501	TSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLT	550
501	TSENXTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS	550
551	KVTEEVVANMPEGLTPDLVQEACESELNEVTGKIAYETKMDLVQTSEVM--	600
551	KVTEAAVSNMPEGLTPDLVQEACESELNEATGKIAYETKVDLVQTSEAI	600

FIG. 13A

SUBSTITUTE SHEET (RULE 26)

1. The first part of the book is a general introduction to the subject of the history of the United States, and is written in a very clear and concise manner. It covers the period from the discovery of the continent to the present time, and gives a good outline of the main events of our history.

WO 00/31235

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PCT/US99/26160

601 QESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSS 650
 |||||
 601 QESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSV 650
 |||||
 651 SPLEASS-VNYESIKHEPENPPPYEEAMSVSLKVSGIKEEIKEPENINAA 700
 |||||
 651 SPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFMAA 700
 |||||
 701 LQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVE 750
 |||||
 701 VQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVE 750
 |||||
 751 DSSPDSEPVDFLSDDSIPDVPQKQDETVMVLVKESLTETSFESMIEYENKE 800
 |||||
 751 DSSPESEPVDFLSDDSIPEVPQTQEEAVMLMKESLTEVS-ETVAQH--KE 800
 |||||
 801 K-LSALPPEGGKPYLESFK--L-SLDNTKDTLLPDEVSTLSKKEKIPLQM 850
 |||||
 801 ERLSASPQELGKPYLESFQPNLHS--TKDAASNDIP-TLTKKEKISLQM 850
 |||||
 851 EELSTAVYSNDDLFIKSEAQIRETETFSOSSPIEIIDEFPTLISSKTDSF 900
 |||||
 851 EEFNTAIYSNDDLSSSKEDKIKESETFSOSSPIEIIDEFPTFVSAKDDSP 900
 |||||
 901 SKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKI 950
 |||||
 901 -KLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPKDEVHV 950
 |||||
 951 SFSDDFSKNGSATS KVL LPPDVSALGHTQAEIESIVKPKVLEKEAEKKL 1000
 |||||
 951 S--DEFSENRSSVSKASISPSNVSALEP-QTEMGSIVKSKSLTKEAEKKL 1000
 |||||
 1001 PSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSL 1050
 |||||
 1001 PSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSL 1050
 |||||
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 |||||
 1051 TVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEV 1100
 |||||
 1101 AISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYV 1150
 |||||
 1101 AISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYV 1150
 |||||
 1151 GALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 1200
 |||||
 1151 GALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQ 1200
 |||||
 1201 AKIPGLKRKAE..... 1250
 |||||
 1201 AKIPGLKRKAD..... 1250

FIG. 13B

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1 CAG GCT TAG TCT GGG GAA GCG GGT GTT TCA TGT CTC AGG GAG
 Q A - S G E A G V S C L R E
 43 AAT TTT GCA GTT TAC AGC GTT TCT GTT GGT ATG CAT AAT TTG
 N F A V Y S V S V G M H N L
 85 TAA TTG CTG CTG GAG GGC AGA TCG TGG CAA GAA ^{START}ATG GAC GGA
 - L L L E G R S W Q E M D G
 127 CAG AAG AAA CAT TGG AAG GAC AAG GTT GTT GAC CTC CTC TAC
 Q K K H W K D K V V D L L Y
 169 TGG AGA GAC ATT AAG AAG ACT GGA GTG GTG TTT GGT GCC AGC
 W R D I K K T G V V F G A S
 211 TTA TTC CTG CTG CTG TCT CTG ACA GTG TTC AGC ATT GTC AGT
 L F L L L S L T V F S I V S
 253 GTA ACG GCC TAC ATT GCC TTG GCC CTG CTC TCG GTG ACT ATC
 V T A Y I A L A L L S V T I
 295 AGC TTT AGG ATA TAT AAG GGC GTG ATC CAG GCT ATC CAG AAA
 S F R I Y K G V I Q A I Q K
 337 TCA GAT GAA GGC CAC CCA TTC AGG GCA TAT TTA GAA TCT GAA
 S D E G H P F R A Y L E S E
 379 GTT GCT ATA TCA GAG GAA TTG GTT CAG AAA TAC AGT AAT TCT
 V A I S E E L V Q K Y S N S
 421 GCT CTT GGT CAT GTG AAC AGC ACA ATA AAA GAA CTG AGG CCG
 A L G H V N S T I K E L R R
 463 CTT TTC TTA GTT GAT GAT TTA GTT GAT TCC CTG AAG TTT GCA
 L F L V D D L V D S L K F A
 505 GTG TTG ATG TGG GTG TTT ACT TAT GTT GGT GCC TTG TTC AAT
 V L M W V F T Y V G A L F N
 547 GGT CTG ACA CTA CTG ATT TTA GCT CTG ATC TCA CTC TTC AGT
 G L T L L I L A L I S L F S

FIG. 14A

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589 ATT CCT GTT ATT TAT GAA CGG CAT CAG GTG CAG ATA GAT CAT
I P V I Y E R H Q V Q I D H

631 TAT CTA GGA CTT GCA AAC AAG AGT GTT AAG GAT GCC ATG GCC
Y L G L A N K S V K D A M A

673 AAA ATC CAA GCA AAA ATC CCT GGA TTG AAG CGC AAA GCA GAT
K I Q A K I P G L K R K A D

715 ^{STOP}
TGA AAA AGC CCC AAA CAG AAG TTC ATC TTT AAA GGG GAC ACT
- K S P K Q K F I F K G D T

757 CAC TTG ATT ACG GGG GTG GGA GGT CAG GGG TGA GCC CTT GGT
H L I T G V G G Q G - A L G

799 GGC CGT GCG GTT TCA GCT CTT TAT TTT TAG CAG TGC ACT GTT
G R A V S A L Y F - Q C T V

841 TGA GGA AAA ATT ACC TGT CTT GAC TTC CTG TGT TTA TCA TCT
- G K I T C L D F L C L S S

883 TAA GTA TTG TAA GCT GCT GTG TAT GGA TCT CAT TGT AGT CAC
- V L - A A V Y G S H C S H

925 ACT TGT CTT CCC CAA TGA GGC GCC TGG TGA ATA AAG GAC TCG
T C L P Q - G A W - I K D S

967 GGG AAA GCT GTG CAT TGT ATC TGC TGC AGG GTA GTC TAG CTG
G K A V H C I C C R V V - L

1009 TAT GCA GAG AGT TGT AAA GAA GGC AAA TCT GGG GGC AGG GAA
Y A E S C K E G K S G G R E

1051 AAC CCT TTT CAC AGT GTA CTG TGT TTG GTC AGT GTA AAA CTG
N P F H S V L C L V S V K L

1093 ATG CAG ATT TTT CTG AAA TGA AAT GTT TAG ATG AGA GCA TAC
M Q I F L K - N V - M R A Y

1135 TAC TAA AGC AGA GTG GAA AAC TCT GTC TTT ATG GTG TGT TCT
Y - S R V E N S V F M V C S

FIG. 14B

1177 AGG TGT ATT GTG AAT TTA CTG TTA TAT TGC CAA TAT AAG TAA
R C I V N L L L Y C Q Y K -

1219 ATA TAG ACC TAA TCT ATA TAT AGT GTT TCA CAA AGC TTA GAT
I - T - S I Y S V S Q S L D

1261 CTT TAA CCT TGC AGC TGC CCC ACA GTG CTT GAC CTC TGA GTC
L - P C S C P T V L D L - V

1303 ATT GGT TAT GCA GTG TAG TCC CAA CCA CAT AAA CTA GGA AGA
I G Y A V - S Q A H K L G R

1345 GAA ATG TAT TTG TAG GAG TGC TAC CTA CCA CCT GTT TTC AAG
E M Y L - E C Y L P P V F K

1387 AAA ATA TAG AAC TCC AAC AAA AAT ATA GAA TGT CAT TTC AAA
K I - N S N K N I E C H F K

1429 GAC TTA CTG TAT GTA TAG TTA ATT TTG TCA CAG ACT CTG AAA
D L L Y V - L I L S Q T L K

1471 TTC TAT GGA CTG AAT TTC ATG CTT CCA AAT GTT TGC AGT TAT
F Y G L N F M L P N V C S Y

1513 CAA ACA TTG TTA TGC AAG AAA TCA TAA AAT GAA GAC TTA TAC
Q T L L C K K S - N E D L Y

1555 CAT TGT GGT TTA AG
H C G L

FIG. 14C

FIG.15A

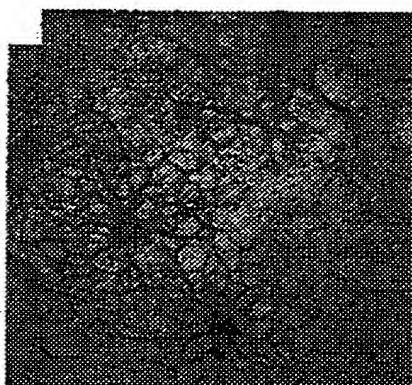


FIG.15B

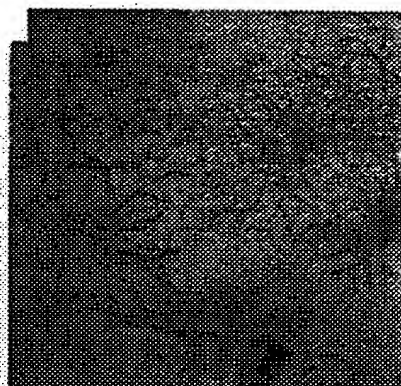


FIG.15C

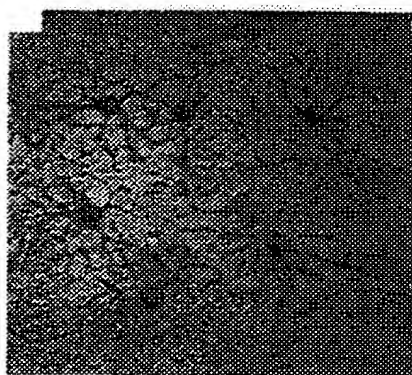


FIG.15D



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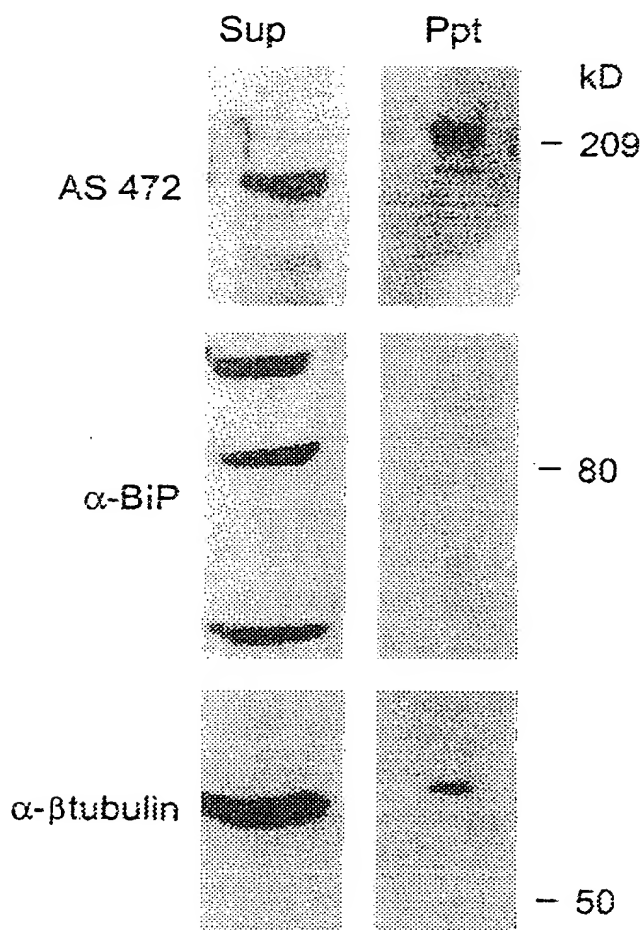


FIG. 15E

FIG.16A

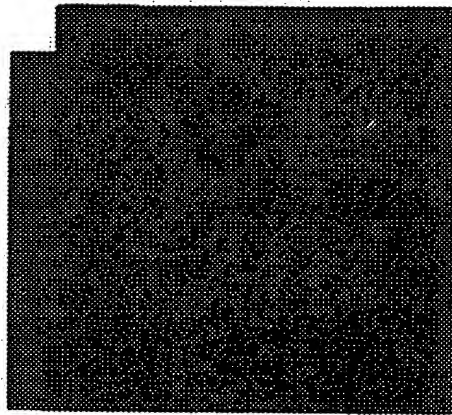


FIG.16B

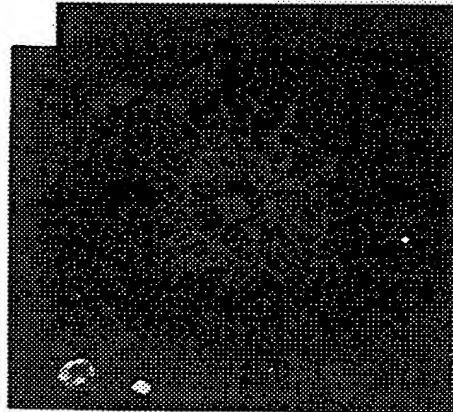
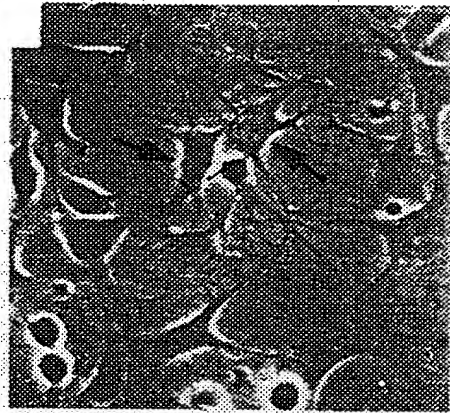


FIG.16C

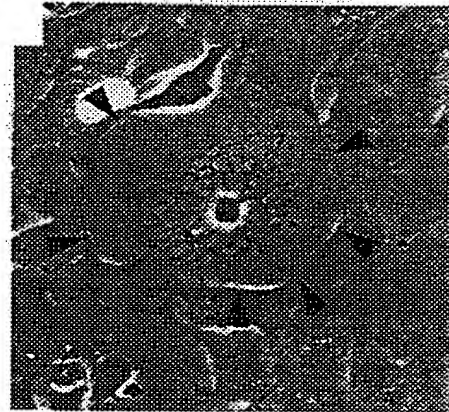


FIG.16D

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FIG. 16E

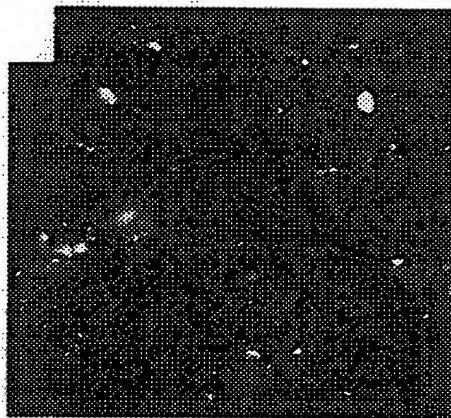


FIG. 16F

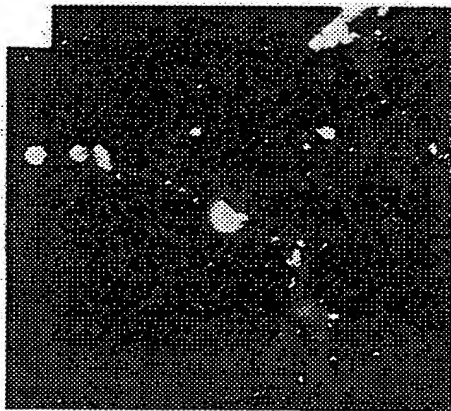
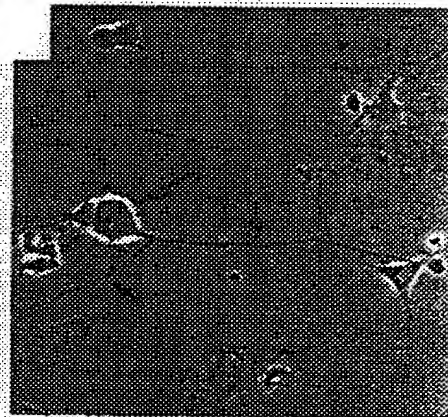


FIG. 16G



FIG. 16H

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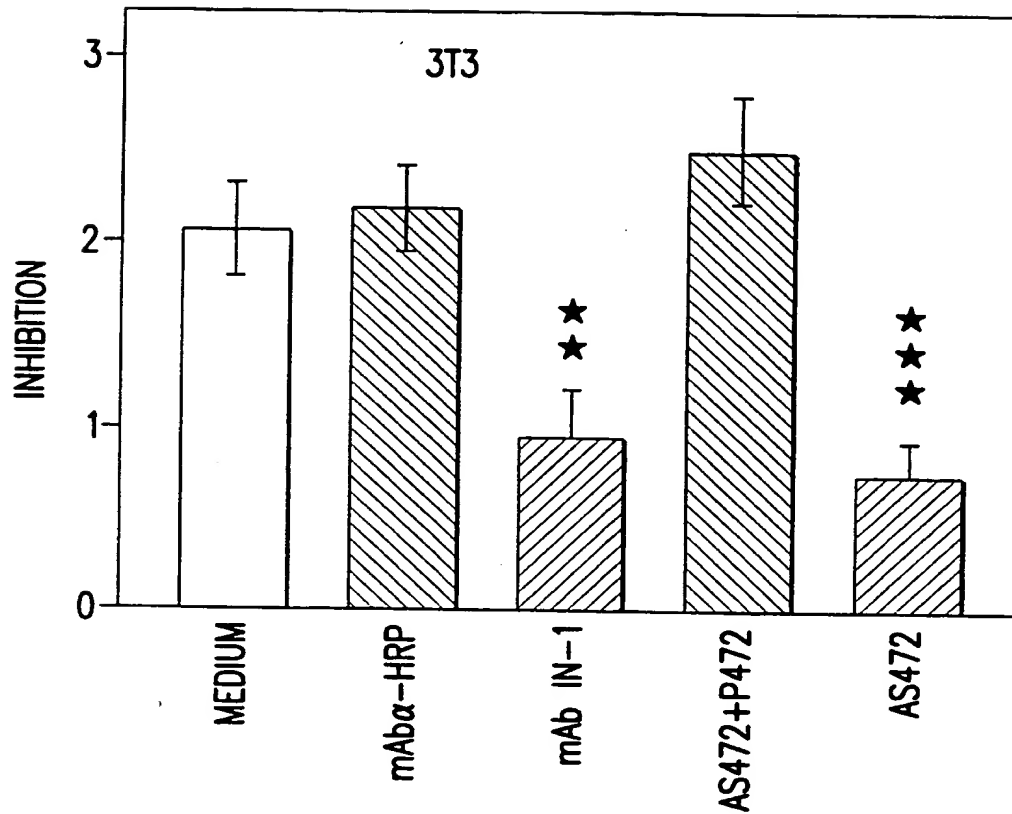


FIG.16I

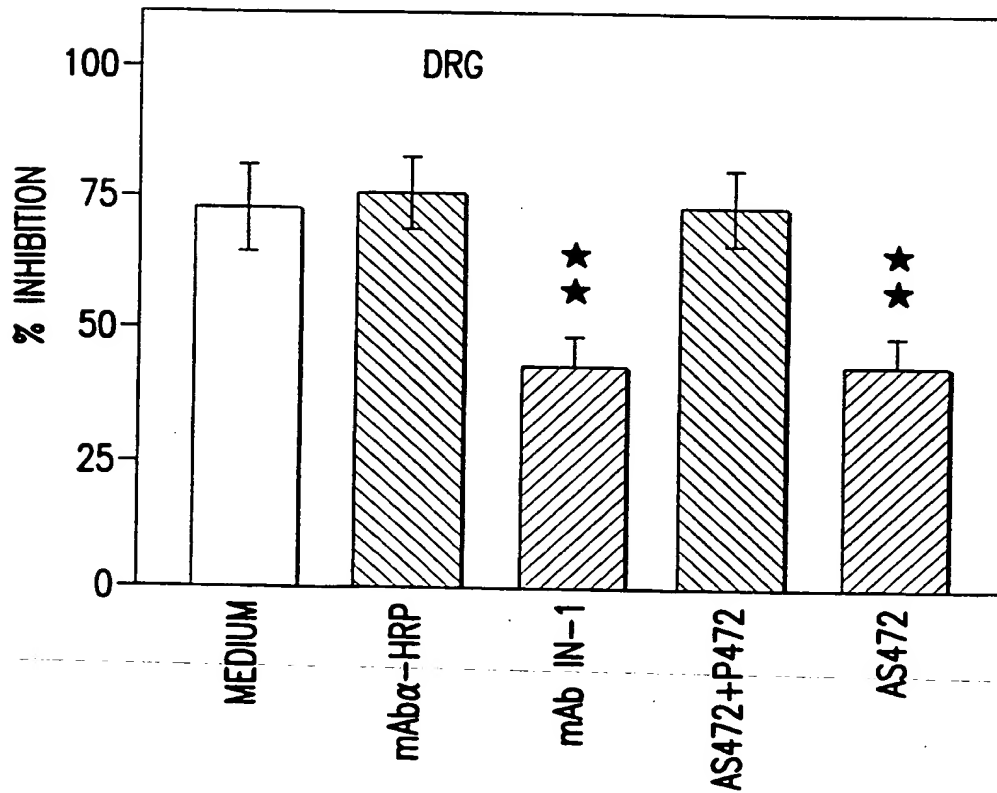


FIG.16J

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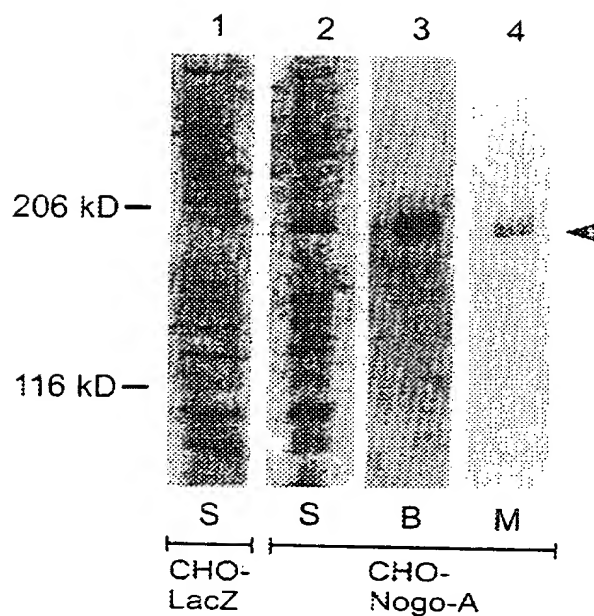


FIG.17A

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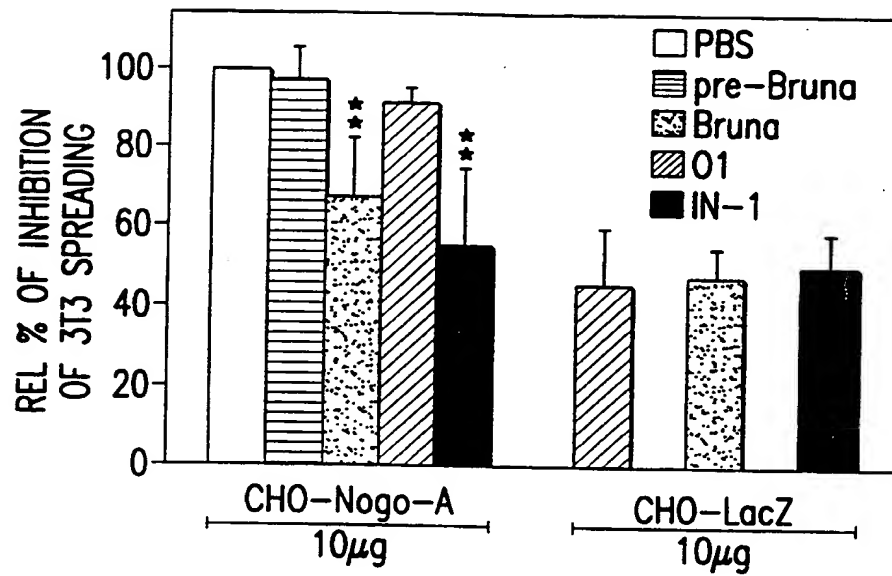


FIG. 17B

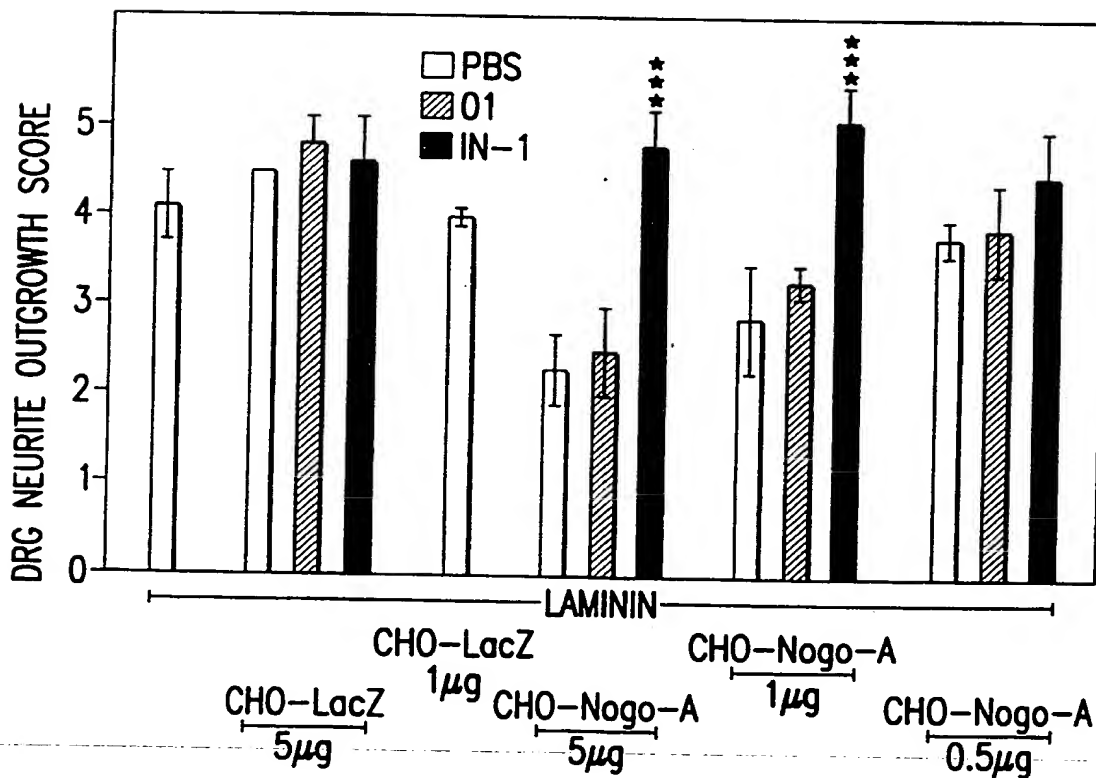


FIG. 17C

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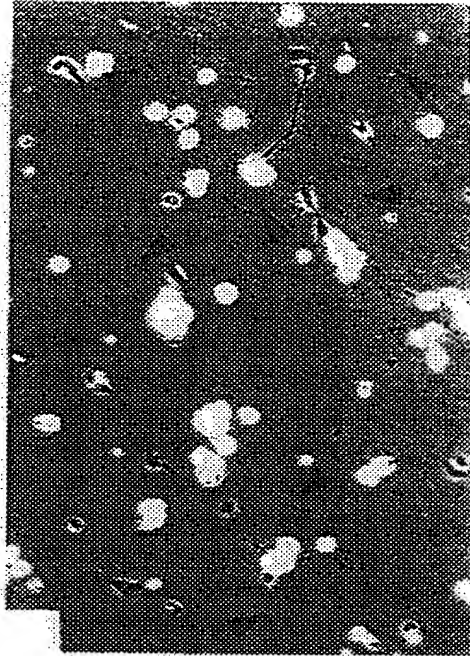


FIG.17E

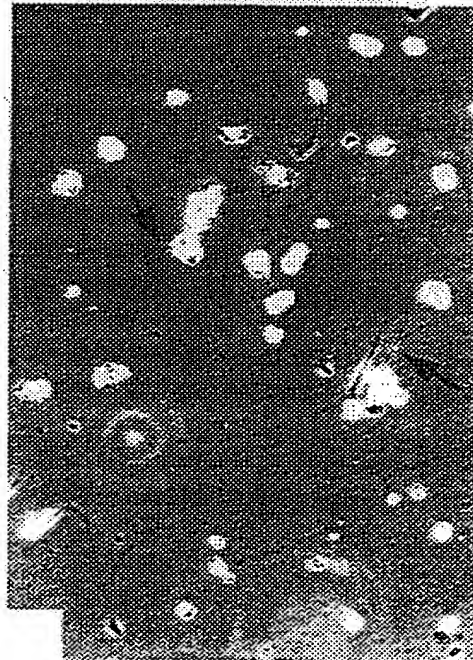
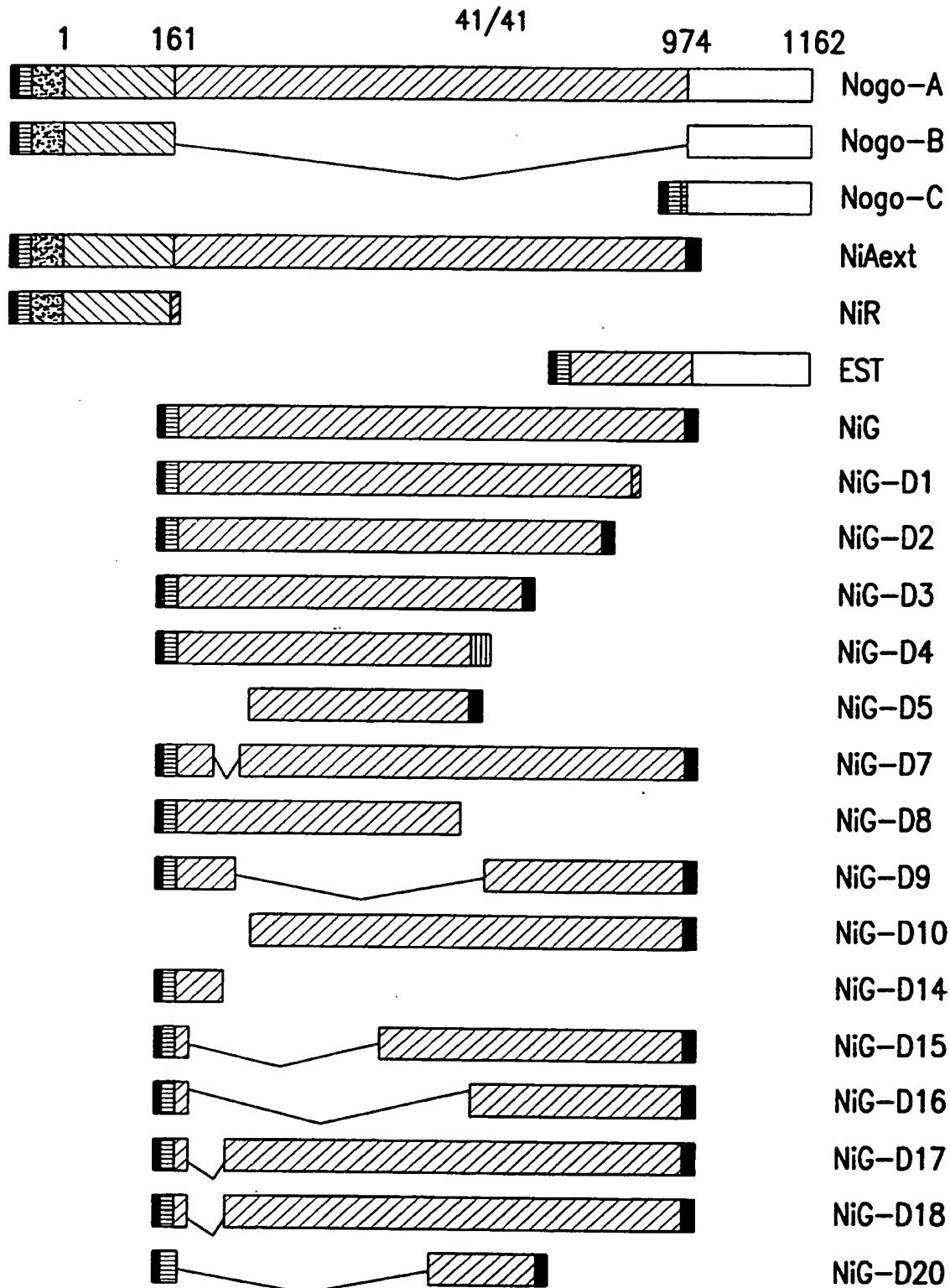


FIG.17D

FIG.17D 2260E850



aa 1-161 SEQ.ID NO.2
 aa 161-974 SEQ.ID NO.2
 aa 974-1162 SEQ.ID NO.2
 His-tag
 N-TERMINAL VECTOR SEQUENCE
 Nogo-C-SPECIFIC N-TERMINAL SEQUENCE
 T7-tag
 C-TERMINAL VECTOR SEQUENCES

FIG. 18